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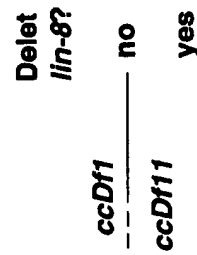
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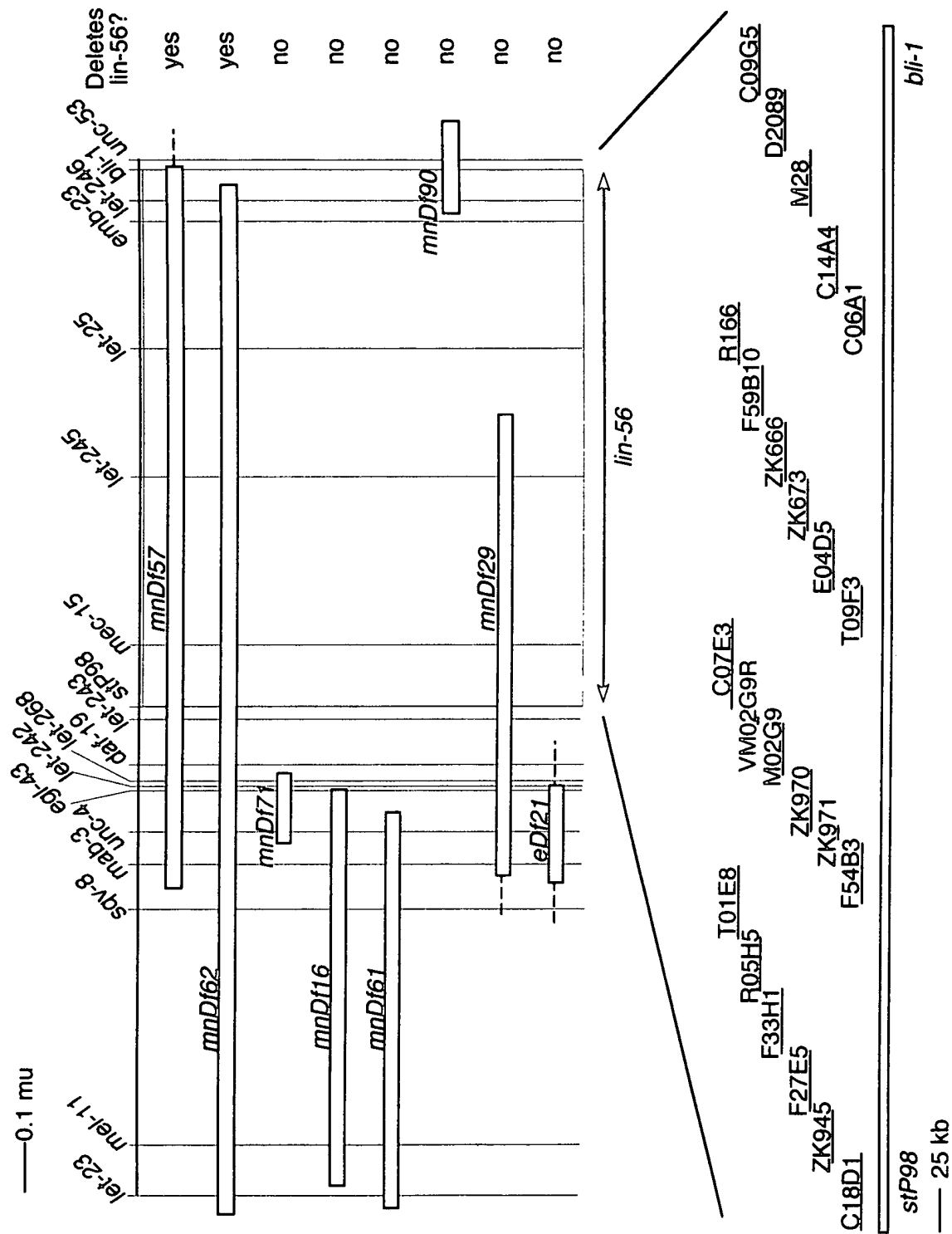
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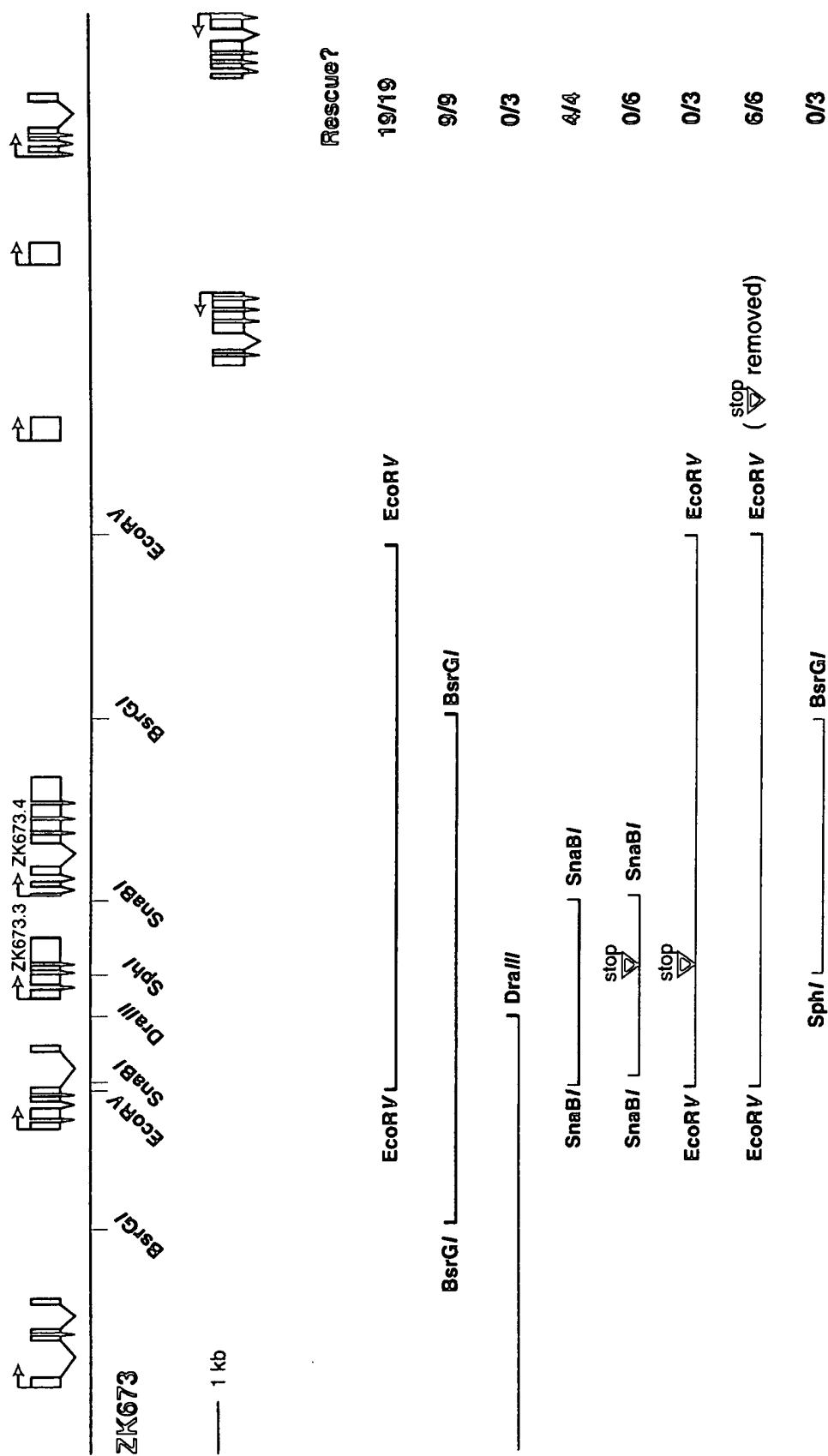
FIG. 3

	$\nabla n111p$	$\nabla n2741M$	
LIN-8	MSKIKTHSTGSKRTVPFYKLPBPVPLPPLPPPDPTRYFSTEKYIALSKDEKFKFDDYDVNDETLKKVVLNEIGKC		75
C41H7.3	MLSTKQE-----LLDAPBPBPAAATPLPPI--THRISLSGYRNI--HAKSFLKTMMDLCVRRVALLSLENR		62
C41H7.4	MSLKQE-----HMHPBPRAITPLPPA--THQITLIEYKER--EKDYRYRDATKDA SVKKVMSLLKDH		60
C41H7.5	MSLKQE-----HMNPBPRTIITPLPPP--THQITIIEYKER--VKRDYRYRNATKDTSLKKVMSLIKDR		60
C41H7.6	MLNTKQE-----GVVADAPRALTIPIPF--IHVSMEEYMG M--ELNSVYEEATKDSALKKKVMDLLKDR		61
C08A9.6	MMNPKEE--PRPFSIVPLPRPRPTTLPPI--SHCITMADYLL--ENTKFHKATATRAPKIKKVLISLLKDR		67
C08A9.7	MVSATRV--PRRSSTTSATAQRTPSPLMPA--SFPITMDEYLEK--ENREFVNVNASKD IAMKRLALTLELY		68
F14D2.2	MSRIKQE-----QVNPPPPRAITPLPPA--THRITMDEYKKR--EKKDYRYRDATKDA SVKKVMSLLKDY		62
		$\nabla n3585H$	
LIN-8	PDIWSSRSQAAMEHYPIVATETYRRITGLLL-----SIKSLKQIYKCGKDNLRNRLRVAIVSKRLTPAQVEAY		143
C41H7.3	RALWIRVHKSPKADWEVLGV-EVFERTGKAV-----SVKQLQRIFLTARDWLRRNLQLYIIQRKMDKLTLD AE		129
C41H7.4	PGMWQNGNRFQPEKWRALGV-DVYQRTGQIV-----RVNDMRKMLVMGKSVLKKKIAICTRDKKLDR AATEKD		127
C41H7.5	KAMWAPAAKPSSEDKWQKLGA-EVFSRTGKVV-----SVTQLRRMLVSSKHVLKTKMSHCITKVKKMDRVST EAY		134
C41H7.6	PGMWQNGNRFQLENWRELGV-DVYQRTGQIVRAELGEVSVDMMHRMFVVGKAVLKQKITVCTIRYKLDRAATEAD		128
C08A9.6	PEIWDRAKQAFSAKNWNQNLGV-EVYERTGIYV-----RSNDLHKMLRTAKVVLKNKLRCTIGIKKLDRAATE TE		134
C08A9.7	PEMWKPGGPMVAKKWQAFGA-EMYRRITGKIY-----RCKDLSHVFTLT KSSIKRKLRTCTILIKRMHRSKTDEE		135
F14D2.2	PDMWQNGNRFQTRKWRALGV-EVYQRTGQIV-----GVDDMRKMFMSGKT V LKQKITFCIRNMKMDRAATEAD		129
	$\nabla n3648H \nabla n2378K \nabla n2378C$	$\nabla n2403K, n2724K, n3607K$	
LIN-8	MWRMEFYGFIRYRYRDYTORWEADLLKDLDVVLGLEARRASKNMEKVDSGELMEPMPMDSTMDMCVEE EP...		214
C41H7.3	LAKWELYPHFIFYRQYLGQFEAHL-----WTGELY-----DDIICD GIMQVEV...		177
C41H7.4	LWYWEYRHFLYYRETLGQFEANL-----RGE-----WTGEDQIQDE--DDIYDGM LDGDL...		178
C41H7.5	LWNWEFYRHFLYYREMLDRFEANL-----RGKQ-----WTGEDQPTDD--DDIICD GIFEVEM...		186
C41H7.6	LQNWFEYRHFYRRETLGQFEANL-----RGEQ-----WTGEDQPADD--DDIYD GIFEVEM...		180
C08A9.6	LWKWEYYPHFIFYRETLGHFEANL-----RGE-----WDGEAHIDDD--DDIYEGYWEADK...		186
C08A9.7	MWKYELYPYFQYRQSIGQFEAKL-----RDEP-----WTGEDQAQED--DDILFDGLFEVEN...		186
F14D2.2	LQNWEYRHFLYYRQTLGKFEAKL-----RGEQ-----WIGEDQVEDDEDVIFDGES		178
	$\nabla n3591K$		
LIN-8	...EEMNQITYQAIRIAREQPERLKLRLKALFDVVLAFDQK--EYADVGDLYRDLAQKNS		386
C41H7.3	...EDSVSYTKITEDLLQKKPHKHRFIRQALFKTIMALDDDEVEYTELADLFGDIAEQSNVVRRLRLQRQQRGRGEQ		366
C41H7.4	...RSAQHIAEQAKRLFLQYPEKSNLIRETMFKTILAFDDPSADYQNVGEIFDDLAAQEA AKKRRAENRAQREQ		331
C41H7.5	...STAEQIGEEIDRLIQLYPQREMLIRQAFFKTIFALEDETVEFSNLGDLFEDLAEQENFKRRRRSRAQRLE		327
C41H7.6	...STAEQIGEEIDRLIQLYPQREMLIRQAFFKTIFALEDETVEFSNLGDLFEDLAEQENFKRRRRSRAQRLE		321
C08A9.6	...NSAQHIGEQVHRLFAQYPERSKLFRETLEKTI LALEEP--EYEHA AEVFTDLAQSETAKRRRRSEATWQNGQ		344
C08A9.7	...KTADNIGDQVKQLFVDHPDRANFFREVLFKTVLELRDP--AFTNAGVFFDEMSSLES AKRRRRSEMNK		331

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F/G. 6

LIN-56

MDHHAMYRTAEFNKTTVRLRLAEFIEKTGQNATIVNMDSFLEFFAYLNPTA	50
PIPTVPEIEKQLLKSPIRCIVCGMETESD SANT SIDNAS IL TATVIG	100
YCRDP SDAVNOIRKESIRACTKH FN SI FHV IFEG LQ IENTYCAHHAKYSL	150
ANRWCKVYTMIRSSLGEQFTKFDVVRNFKSILQSFLDTFCEIDDDKKDKES	200
SHFDECFEEMDSENV EIK MESPQEEAAEKS K FSENLVEVKLEPIETHELD	250
KTISDFSSSDIIDSQKLQQNGCFPEKVEQMDKYSNKLKDEASDKKYEKPG	300
KKDYVEEEGYWAPITDSEDD EA	322

69	R	V	G	M	E	T	S	D	S	A	V	T	S	I	D	N	A	S	I	L	T	A	T	V	I	G	Y	C	R	D	P	S	D	A	V	N	Q	T	R	K	E	S	L	R	A	T	K	F	N	S	I	F	128			
211	P	L	E	K	A	L	M	R	E	S	I	A	M	T	D	N	E	A	V	K	V	L	M	A	A	V	M	S	G	H	F	R	M	A	T	A	E	K	A	T	R	H	E	R	L	M	Y	D	V	D	F	V	Y	270		
176	P	I	G	N	E	V	P	G	H	R	S	I	R	V	S	D	D	A	A	F	L	T	A	A	V	L	T	D	Q	K	T	I	R	Q	A	K	R	D	I	L	S	E	Y	E	T	V	L	R	S	L	H	Y	Y	235		
274	P	L	V	N	Q	M	E	M	T	K	V	R	S	V	N	N	T	D	A	Y	I	M	I	Y	V	C	V	M	N	D	K	Y	D	M	D	K	A	K	E	L	A	R	M	Q	R	F	K	C	V	S	L	D	E	L	Y	333

FIG. 7

		10	20	30	40
	****
consensus	1	FDWEDYL---	EETGARAAPVELF---	DKQPVDSPPN	GFKV 34
lin-61	146	VNYVNNCi-	dGEIVGQTSLS	PKF---	DEGKALLSKHRFKV 181
lin-61	23	YLWESYLh	qfEKGKTSFIP	VEAF---	NRNLTVNPN
lin-61	388	FRWDEYL---	EKESAETLPLDLF---	KPMPSQERLD	KFKV 421
hl(3)mbt	206	WSWESYL---	EEQKAITAPVSL	Fq--DSQAVTH	NKNGFKL 240
hl(3)mbt	314	FSWSQYM---	CSTRAQAAPKHM	F---VSQSHSP	PPLGFQV 347
hl(3)mbt	422	FCWEKYL---	EETGASAVPTWAF	-----	KVRPPHSFLV 451
tumor sup(Dm)	819	FRWSEYLk-	SKGKDVAAPIHL	F---LNPFPIS	PNCFEI 852
tumor sup(Dm)	926	FSWSRYL---	VKTGGKAAPRAL	FghlNMQQQM	DVRNGFAV 962
tumor sup(Dm)	1035	FIWDDYI---	SEVGGMAASKEL	F-----	TPRQPMFYQE 1064
scmh1 (mouse)	28	FTWDKYL---	KETCSVPAPVHC	F---KQSYTPP	SPNEFKI 60
scml2 (human)	139	SSWPMFLl-	ktLNGSEMASAT	Lf---KKEPPK	PPLNNFKV 174
		50	60	70	80
	****
consensus	35	-----	GMKLEAVDP-----	RNPSLICVATV	VEVKGYR 61
lin-61	182	-----	GQRLELLNY-----	SNSTEIRVAR	IQEICGRR 208
lin-61	60	-----	GVIFETVVHdy	kncDSIQVRWF	ARIEKVC
lin-61	422	iliskrvGL	RLEAADM-----	CENQFICPAT	VKSVBGRL 455
hl(3)mbt	241	-----	GMKLEGIDP-----	QHPSMYFIL	TVAEVC
hl(3)mbt	348	-----	GMKLEAVDR-----	MNPSLVCSA	SVTDVDSR 374
hl(3)mbt	452	-----	NMKLEAVDR-----	RNPALIRVA	SVEDVEDHR 478
tumor sup(Dm)	853	-----	GMKLEAIDP-----	ENCSLFCVC	SIVEVRGYR 879
tumor sup(Dm)	963	-----	GMHLEAEDL-----	NDTGKICVAT	VTDILDER 989
tumor sup(Dm)	1065	-----	RMKLEVVDQ-----	RNPCLIRPAT	VVTRKGYR 1091
scmh1 (mouse)	61	-----	SMKLEAQDP-----	RNTTSTCIAT	VVGLTGAR 87
scml2 (human)	175	-----	GMKLEAIDK-----	KNPYLICPAT	IGDVKGDE 201
		90	100	110	120
	****
consensus	62	LLLHFD-----	GWDDR-----	YDFWCDADSP	DIF 85
lin-61	209	MNVSITk	kdfpeslpdADDD	Rqvfs	sgSQYWIDEGS
lin-61	93	VLAQFI-----	GAD-----	TKFWLNILS	DDMF 114
lin-61	456	INVNFD-----	GWDEE-----	FDELYDVDS	SHDIL 479
hl(3)mbt	268	LRLHFD-----	GYSEC-----	HDFWVNANS	PDII 291
hl(3)mbt	375	FLVHFD-----	NWDDT-----	YDYWCDPSS	PYIH 398
hl(3)mbt	479	IKIHFD-----	GWSHG-----	YDFWIDADH	PDII 502
tumor sup(Dm)	880	LKLSFD-----	GYSSM-----	YDFWVNADS	QDIF 903
tumor sup(Dm)	990	IRVHFD-----	GWDDC-----	YDLWVHITS	PYIH 1013
tumor sup(Dm)	1092	VQLHLD-----	CWPT-----	YYFWLEDD	SPDLH 1115
scmh1 (mouse)	88	LRLRLD-----	GSDNK-----	NDFWRLVDS	SSEIQ 111
scml2 (human)	202	VHITFD-----	GWGA-----	FDYWCKYDS	RDIF 225
		130			
	**		
consensus	86	PVGWCEKNGH	PLQPP 100		
lin-61	249	PVGFAAVNGY	QLNAK 263		
lin-61	115	GLANAAM-	SDPNMDK 128		
lin-61	480	PIGWCEAHSY	VLQPP 494		
hl(3)mbt	292	PAGWFEKTGH	KLQLP 306		
hl(3)mbt	399	PVGWCQKQGK	PLTPP 413		
hl(3)mbt	503	PAGWCSKTGH	PLQPP 517		
tumor sup(Dm)	904	PPGWCEDETA	RVLQAP 918		
tumor sup(Dm)	1014	PCGWHEGRQ	QLIVPP 1028		
tumor sup(Dm)	1116	PIGWCEATS	SHELETP 1130		
scmh1 (mouse)	112	PIGNCEKNGG	MQLQPP 126		
scml2 (human)	226	PAGWCRLTGD	VLQPP 240		

SCANNED, # 20

Model	Model	Model	Model
Model 1	Model 2	Model 3	Model 4
Model 5	Model 6	Model 7	Model 8
Model 9	Model 10	Model 11	Model 12
Model 13	Model 14	Model 15	Model 16
Model 17	Model 18	Model 19	Model 20
Model 21	Model 22	Model 23	Model 24
Model 25	Model 26	Model 27	Model 28
Model 29	Model 30	Model 31	Model 32
Model 33	Model 34	Model 35	Model 36
Model 37	Model 38	Model 39	Model 40
Model 41	Model 42	Model 43	Model 44
Model 45	Model 46	Model 47	Model 48
Model 49	Model 50	Model 51	Model 52
Model 53	Model 54	Model 55	Model 56
Model 57	Model 58	Model 59	Model 60
Model 61	Model 62	Model 63	Model 64
Model 65	Model 66	Model 67	Model 68
Model 69	Model 70	Model 71	Model 72
Model 73	Model 74	Model 75	Model 76
Model 77	Model 78	Model 79	Model 80
Model 81	Model 82	Model 83	Model 84
Model 85	Model 86	Model 87	Model 88
Model 89	Model 90	Model 91	Model 92
Model 93	Model 94	Model 95	Model 96
Model 97	Model 98	Model 99	Model 100

438	Translation of lin-61 cDNA	433	RL	F	D	G	N	E	E	F	E	L	V	D	S	K	N	D	L	P	G	N	C	L	A	E	H	V	L	O	P	P	K	K	Y	N	Y	438
439	Protein product of hsp HA90918.9	434	RL	R	F	D	G	N	E	E	F	E	L	V	D	S	K	N	D	L	P	G	N	C	L	A	E	H	V	L	O	P	P	K	K	Y	439	
440	Protein product of Ce Y4801A.a	435	RL	R	F	D	G	N	E	E	F	E	L	V	D	S	K	N	D	L	P	G	N	C	L	A	E	H	V	L	O	P	P	K	K	Y	440	
441	Protein product of Ce Y4801A.a	436	RL	R	F	D	G	N	E	E	F	E	L	V	D	S	K	N	D	L	P	G	N	C	L	A	E	H	V	L	O	P	P	K	K	Y	441	
442	Protein product of Ce Y4801A.a	437	RL	R	F	D	G	N	E	E	F	E	L	V	D	S	K	N	D	L	P	G	N	C	L	A	E	H	V	L	O	P	P	K	K	Y	442	
443	Protein product of Ce Y4801A.a	438	RL	R	F	D	G	N	E	E	F	E	L	V	D	S	K	N	D	L	P	G	N	C	L	A	E	H	V	L	O	P	P	K	K	Y	443	
444	Protein product of Ce Y4801A.a	439	RL	R	F	D	G	N	E	E	F	E	L	V	D	S	K	N	D	L	P	G	N	C	L	A	E	H	V	L	O	P	P	K	K	Y	444	
445	Protein product of Ce Y4801A.a	440	RL	R	F	D	G	N	E	E	F	E	L	V	D	S	K	N	D	L	P	G	N	C	L	A	E	H	V	L	O	P	P	K	K	Y	445	
446	Protein product of Ce Y4801A.a	441	RL	R	F	D	G	N	E	E	F	E	L	V	D	S	K	N	D	L	P	G	N	C	L	A	E	H	V	L	O	P	P	K	K	Y	446	
447	Protein product of Ce Y4801A.a	442	RL	R	F	D	G	N	E	E	F	E	L	V	D	S	K	N	D	L	P	G	N	C	L	A	E	H	V	L	O	P	P	K	K	Y	447	
448	Protein product of Ce Y4801A.a	443	RL	R	F	D	G	N	E	E	F	E	L	V	D	S	K	N	D	L	P	G	N	C	L	A	E	H	V	L	O	P	P	K	K	Y	448	
449	Protein product of Ce Y4801A.a	444	RL	R	F	D	G	N	E	E	F	E	L	V	D	S	K	N	D	L	P	G	N	C	L	A	E	H	V	L	O	P	P	K	K	Y	449	
450	Protein product of Ce Y4801A.a	445	RL	R	F	D	G	N	E	E	F	E	L	V	D	S	K	N	D	L	P	G	N	C	L	A	E	H	V	L	O	P	P	K	K	Y	450	
451	Protein product of Ce Y4801A.a	446	RL	R	F	D	G	N	E	E	F	E	L	V	D	S	K	N	D	L	P	G	N	C	L	A	E	H	V	L	O	P	P	K	K	Y	451	
452	Protein product of Ce Y4801A.a	447	RL	R	F	D	G	N	E	E	F	E	L	V	D	S	K	N	D	L	P	G	N	C	L	A	E	H	V	L	O	P	P	K	K	Y	452	
453	Protein product of Ce Y4801A.a	448	RL	R	F	D	G	N	E	E	F	E	L	V	D	S	K	N	D	L	P	G	N	C	L	A	E	H	V	L	O							

FIG. 9A



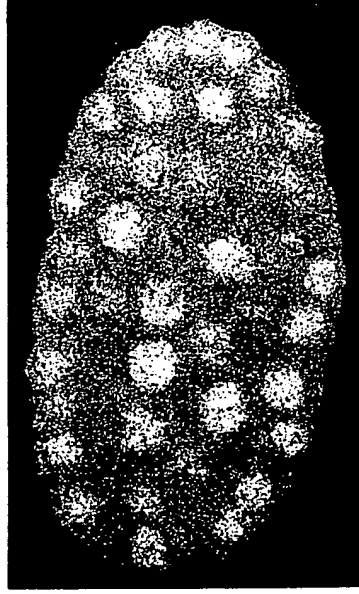
2-cell embryo

FIG. 9B



4-cell embryo

FIG. 9C



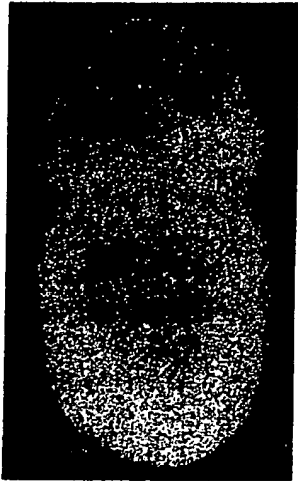
multicellular embryo

FIG. 9D



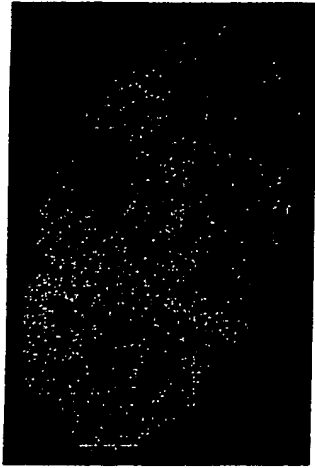
vulval region of an L4 larva

FIG. 10A



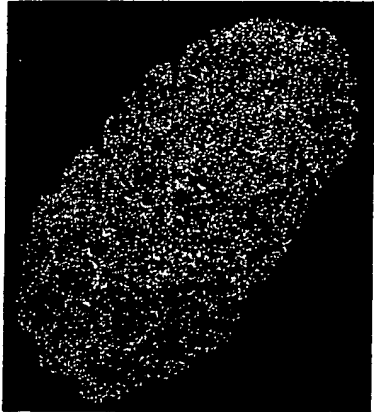
2-cell embryo

FIG. 10B



4-cell embryo

FIG. 10C



multicellular embryo

FIG. 10D



vulval region of an L4 larva

FIG.11A



FIG.11B

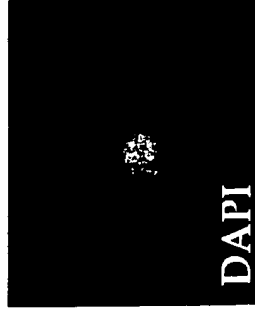
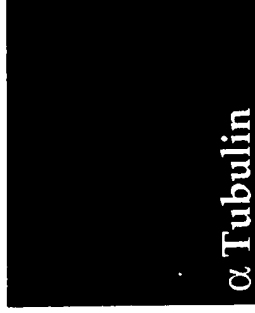


FIG.11C



α Tubulin

DAPI

FIG. 12A



FIG. 12B

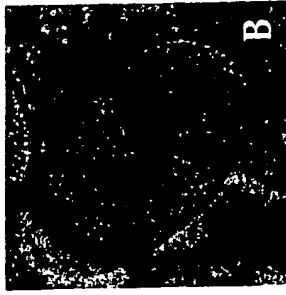


FIG. 12C

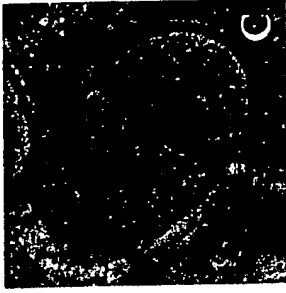


FIG. 12D



FIG. 12E

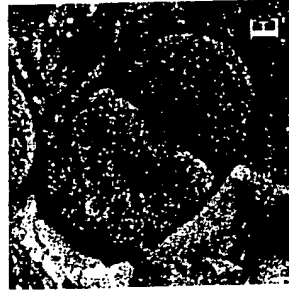


FIG. 12F

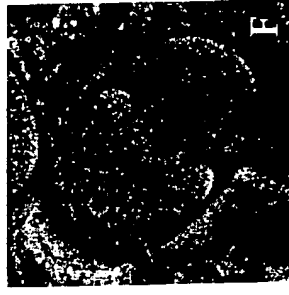


FIG. 12G



FIG. 12H



FIG. 13A

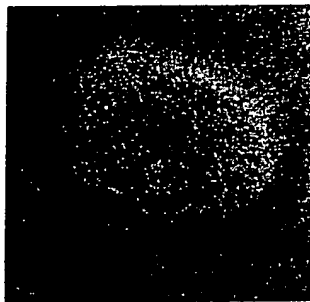


FIG. 13B

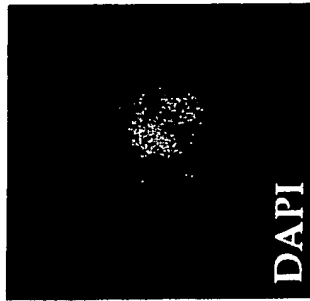


FIG. 13C

